

Sound

1646

#12

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/765,588

DATE: 09/01/98
TIME: 16:14:03

Input Set: H765588.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

new format

ENTERED

1 <110> APPLICANT: Hayward, Nicholas K.
2 Weber, Gunther
3 Grimmond, Sean
4 Nordenskjold, Magnus
5 Larsson, Catharina
6 <120> TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
7 SAME
8 <130> FILE REFERENCE: DAVIES
9 <140> CURRENT APPLICATION NUMBER: US/08/765,588
10 <141> CURRENT FILING DATE: 1997-04-25
11 <160> NUMBER OF SEQ ID NOS: 23
12 <170> SOFTWARE: PatentIn Ver. 2.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 649
15 <212> TYPE: DNA
16 <213> ORGANISM: Nucleotide Sequence of VEGF165
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19 <222> LOCATION: (17)..(589)
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23 1 5 10
24 gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100
25 Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
26 15 20 25
27 atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148
28 Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
29 30 35 40
30 gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196
31 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
32 45 50 55 60
33 atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244
34 Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
35 65 70 75
36 tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg 292
37 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
38 80 85 90
39 gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg 340
40 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
41 95 100 105
42 atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag 388
43 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
44 110 115 120

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47      125                      130                      135                      140
48      aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa      484
49      Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
50      145                      150                      155
51      gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc      532
52      Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
53      160                      165                      170
54      aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag      580
55      Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
56      175                      180                      185
57      ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgtttcgg      629
58      Pro Arg Arg
59      190
60      gaaccagatc tctcaccagg      649
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63      <212> TYPE: PRT
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69      20                      25                      30
70      Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
71      35                      40                      45
72      Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
73      50                      55                      60
74      Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
75      65                      70                      75                      80
76      Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
77      85                      90                      95
78      Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
79      100                      105                      110
80      Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
81      115                      120                      125
82      Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
83      130                      135                      140
84      Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
85      145                      150                      155                      160
86      Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
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91      <211> LENGTH: 1094
92      <212> TYPE: DNA
93      <213> ORGANISM: Nucleotide Sequence of SOM175
94      <220> FEATURE:

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100      1          5          10          15
101   ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac   95
102   Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
103      20          25          30
104   cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc   143
105   Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
106      35          40          45
107   cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc   191
108   Gln Pro Arg Glu Val Val Val Leu Thr Val Glu Leu Met Gly Thr
109      50          55          60
110   gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt   239
111   Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
112      65          70          75
113   ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac   287
114   Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
115      80          85          90          95
116   caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg   335
117   Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
118      100         105         110
119   ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa   383
120   Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
121      115         120         125
122   aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac   431
123   Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His
124      130         135         140
125   cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca   479
126   Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala
127      145         150         155
128   ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct   527
129   Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser
130      160         165         170         175
131   gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc   575
132   Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala
133      180         185         190
134   gct gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct   623
135   Ala Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
136      195         200         205
137   tagagctcaa cccagacacc tgcaggtgcc ggaagctgcg aaggtgacac atggcttttc 683
138   agactcagca gggtagcttg cctcagaggc tatatcccag tgggggaaca aaggggagcc 743
139   tggtaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803
140   ggcctctcag agggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863
141   agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct caggggagaa 923
142   tggagtactg tctcagtttc taaccactct gtgcaagtaa gcatcttaca actggctctt 983
143   cctcccctca ctaagaagac ccaaacctct gcataatggg atttgggctt tgggtacaaga 1043
144   actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a 1094

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153 20 25 30
154 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
155 35 40 45
156 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
157 50 55 60
158 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
159 65 70 75 80
160 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
161 85 90 95
162 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
163 100 105 110
164 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
165 115 120 125
166 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
167 130 135 140
168 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
169 145 150 155 160
170 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
171 165 170 175
172 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
173 180 185 190
174 Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
175 195 200 205
176 <210> SEQ ID NO 5
177 <211> LENGTH: 993
178 <212> TYPE: DNA
179 <213> ORGANISM: Nuc. Seq. of SOM175 Absent Exon 6
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182 <222> LOCATION: (3)..(566)
183 <400> SEQUENCE: 5
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186 1 5 10 15
187 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
188 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
189 20 25 30
190 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
191 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
192 35 40 45
193 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
194 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr

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198          65          70          75
199  ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
200  Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
201  80          85          90          95
202  caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
203  Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
204          100          105          110
205  ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
206  Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
207          115          120          125
208  aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca 431
209  Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro
210          130          135          140
211  cgc tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc 479
212  Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys
213          145          150          155
214  cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag 527
215  Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
216  160          165          170          175
217  ctc aac cca gac acc tgc agg tgc cgg aag ctg cga agg tgacacatgg 576
218  Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
219          180          185
220  cttttcagac tcagcagggt gacttgccctc agaggctata tcccagtgagg ggaacaaaagg 636
221  ggagccttgtt aaaaaacagc caagcccccac agacctcagc ccaggcagaa gctgctctag 696
222  gacctggggcc tctcagagggt ctcttctgcc atcccttgctc tccctgaggc catcatcaaaa 756
223  caggacagag ttggaagagg agactggggag gcagcaagag gggtcacata ccagctcagg 816
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225  gctcttcctc ccctcactaa gaagacccaa acctctgcat aatgggattt gggcttttgt 936
226  acaagaactg tgacccccaa ccctgataaa agagatggaa ggaaaaaaaa aaaaaaa 993
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235          20          25          30
236  Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
237          35          40          45
238  Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
239          50          55          60
240  Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
241  65          70          75          80
242  Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
243          85          90          95
244  Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly

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VERIFICATION SUMMARY
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